gnl|CDD|8102, pfam01715, IPPT, IPP transferase. This is a family of IPP transferases EC:2.5.1.8 also known as tRNA delta(2)-isopentenylpyrophosphate transferase. These enzymes modify both cytoplasmic and mitochondrial tRNAs at A(37) to give isopentenyl A(37).

```
              CD-Length = 253 residues,  90.5% aligned
              Score =  173 bits (441), Expect = 3e-44

Query:  51   MQVYEGLDIITNKVSAQEQRICRHHMISFVDPLVTNYTVVDFRNRATALIEDIFARDKIP  110
Sbjct:  1    MQVYKGMDIGTAKPSLEEREGVPHHLIDILDPTES-YSAAEFQRDALEAIAEIRARGKIP  59

Query:  111  IVVGGTNYYIESLLWKVLVNTKPQEMGTEKVIDRKVE--LEKEDGLVLHKRLSQVDPEMA  168
Sbjct:  60   LLVGGTGLYFKALLDGL-----SDTPAADPKVRAKLEEQLEELGNDYLHAELASVDPEAA  114

Query:  169  AKLHPHDKRKVARSLQVFEETGISHSEFLHRQHTEEGGGPLGGPLKFSNPCILWLHADQA  228
Sbjct:  115  AKIHPNDGRRIVRALEVFYATGKPISEFQKEQKNAL----------PYDIVQIGLARDRE  164

Query:  229  VLDERLDKRVDDMLAAGLLEELRDFHRRYNQKNVSENSQDYQHGIFQSIGFKEFHEYLIT  288
Sbjct:  165  VLHERIARRVDDMLESGLVEEVKALYAQGLNEDL---------PSIRAIGYKEFLLYL--  213

Query:  289  EGKCTLETSNQLLKKG  304
Sbjct:  214  DGECTLEEAIERIIKN  229
```

gnl|CDD|405, smart00451, ZnF_U1, U1-like zinc finger; Family of C2H2-type zinc fingers, present in matrin, U1 small nuclear ribonucleoprotein C and other RNA-binding proteins.

```
              CD-Length = 35 residues,  91.4% aligned
              Score = 37.1 bits (86), Expect = 0.004

Query:  363  HLCDLCDRIIIGDREWAAHIKSKSHLNQLKKR  394
Sbjct:  4    FYCKLCNVTFTDEISVEAHLKGKKHKKNVKKR  35
```

gnl|CDD|8115, pfam01745, IPT, Isopentenyl transferase. Isopentenyl transferase / dimethylallyl transferase synthesises isopentenyladensosine 5'-monophosphate, a cytokinin that induces shoot formation on host plants infected with the Ti plasmid.

```
              CD-Length = 233 residues, only  16.7% aligned
              Score = 36.8 bits (85), Expect = 0.005

Query:  19   LVVILGATGTGKSTLALQLGQRLGGEIVSADSMQVYEGL  57
Sbjct:  3    LYLIWGATCTGKTAEAIALAKSTGWPVIVLDRVQCCSQL  41
```

gnl|CDD|10515, COG0645, COG0645, Predicted kinase [General function prediction only]

```
              CD-Length = 170 residues, only  18.2% aligned
              Score = 36.5 bits (84), Expect = 0.007

Query:  19   LVVILGATGTGKSTLALQLGQRLGGEIVSAD  49
Sbjct:  3    LVLVGGLPGSGKSTLARGLAELLGAIRLRSD  33
```

**Help** | Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

L4 ANSWER 5 OF 6 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 2001:784384 SCISEARCH
THE GENUINE ARTICLE: 476WV
TITLE: Regulation of physiological rates in Caenorhabditis elegans by a tRNA-modifying enzyme in the mitochondria
AUTHOR: Lemieux J; Lakowski B; Webb A; Meng Y; Ubach A; Bussiere F; Barnes T; Hekimi S (Reprint)
CORPORATE SOURCE: McGill Univ, Dept Biol, 1205 Doctor Penfield Ave, Montreal, PQ H3A 1B1, Canada (Reprint); McGill Univ, Dept Biol, Montreal, PQ H3A 1B1, Canada
COUNTRY OF AUTHOR: Canada
SOURCE: GENETICS, (SEP 2001) Vol. 159, No. 1, pp. 147-157.
Publisher: GENETICS, 428 EAST PRESTON ST, BALTIMORE, MD 21202 USA.
ISSN: 0016-6731.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 39

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB We show that the phenotype associated with gro-1(e2400) comprises the whole suite of features that characterize the phenotype of the dl mutants in Caenorhabditis elegans, including deregulated developmental, behavioral, and reproductive rates, as well as increased life span and a maternal effect. We cloned gro-1 and found that it encodes a highly conserved cellular enzyme, isopentenylpyroptiosphate:tRNA transferase (IPT), which modifies a subset of tRNTAs. In yeast, two forms of the enzyme are produced by alternative translation initiation, oric of which is mitochondrial. In the gro-1 transcript there are also two possible initiator ATGs, between which there is a sequence predicted to encode a mitochondrial localization signal. A functional GRO-1::GFP fusion protein is localized diffusely throughout the cytoplasm and nucleus. A GRO-1:GFP initiated from the first methionine is localized exclusively to the mitochondria and rescues the mutant phenotype. In contrast, a protein initiated from the second methionine is localized diffusely throughout the cell and does not rescue the mutant phenotype. As oxygen consumption and ATP concentration have been reported to be unaffected in gro-1 mutants, our observations suggest that GRO-1 acts in mitochondria and regulates global physiology by unknown mechanisms.

L4 ANSWER 2 OF 6 SCISEARCH COPYRIGHT 2003 THOMSON ISI
ACCESSION NUMBER: 2002:441430 SCISEARCH
THE GENUINE ARTICLE: 552EV
TITLE: Allelic polymorphisms in the Fc gamma RIIC gene can influence its function on normal human natural killer cells
AUTHOR: Ernst L K; Metes D; Herberman R B; Morel P A (Reprint)
CORPORATE SOURCE: Univ Pittsburgh, Inst Canc, Pittsburgh, PA USA (Reprint); Univ Pittsburgh, Dept Pathol, Pittsburgh, PA USA; Univ Pittsburgh, Dept Surg, Pittsburgh, PA USA; Univ Pittsburgh, Dept Med, Pittsburgh, PA USA; Univ Pittsburgh, Dept Mol Genet & Biochem, Pittsburgh, PA USA
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF MOLECULAR MEDICINE-JMM, (APR 2002) Vol. 80, No. 4, pp. 248-257.
Publisher: SPRINGER-VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010 USA.
ISSN: 0946-2716.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 31

*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*

AB Natural killer (NK) cells are important in host defense against viruses and tumors and can induce death of virally infected cells following engagement of cell surface receptors. Human NK cells express receptors for the Fc portion of IgG which stimulate antibody-dependent cell-mediated cytotoxicity and induce cytokine production. We have shown that NK cells from certain individuals can express, in addition to CD16 (FcgammaRIIIa), isoforms of CD32 (FcgammaRIIc 1-4). Expression of CD32 on NK cells is dependent on an allelic polymorphism of the FcgammaRIIC gene. We analyzed the expression and function of CD32 on NK cells from 31 normal donors. Fourteen of the 31 (45%) donors expressed CD32 on their NK cells. Molecular characterization of FcgammaRIIc isoforms expressed by the CD32(+) donors revealed that the majority of donors expressed the FcgammaRIIc 1 isoform. Interestingly, 3 of the 14 positive donors did not express FcgammaRIIc 1, and we identified a novel isoform, FcgammaRIIc5, expressed by these individuals. The expression of this isoform was correlated to a second allelic polymorphism that controls exon splicing. One of the three was found to express FcgammaRIIb on the NK cells. Biochemical analysis revealed that CD32(+) donors of both types expressed a 40-kDa protein, specifically immunoprecipitated by anti-CD32 monoclonal antibodies. Functionally, only individuals expressing the FcgammaRIIc 1 isoform were able to trigger reverse antibody-dependent cell-mediated cytotoxicity via CD32 whereas a CD32(+) individual expressing the FcgammaRIIb isoform was unable to trigger this function. These results demonstrate that the presence of multiple allelic polymorphisms in the FcgammaRIIC gene determine the expression and function of CD32 on NK cells.

# NCBI Conserved Domain Search

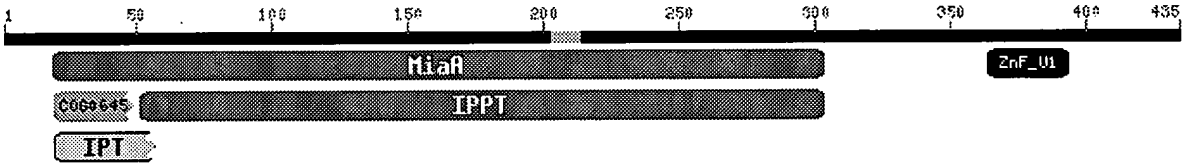


**RPS-BLAST 2.2.6 [Apr-09-2003]**

**Query=** lcl|tmpseq_0
(435 letters)

**Database:** cdd.v1.62
11,088 PSSMs; 2,717,223 total columns

Click on boxes for multiple alignments




Show Domain Relatives

| PSSMs producing significant alignments: | | Score (bits) | E value |
|---|---|---|---|
| gnl\|CDD\|10198 | COG0324, MiaA, tRNA delta(2)-isopentenylpyrophosphate transfer... | 226 | 5e-60 |
| gnl\|CDD\|8102 | pfam01715, IPPT, IPP transferase. This is a family of IPP tran... | 173 | 3e-44 |
| gnl\|CDD\|405 | smart00451, ZnF_U1, U1-like zinc finger; Family of C2H2-type z... | 37.1 | 0.004 |
| gnl\|CDD\|8115 | pfam01745, IPT, Isopentenyl transferase. Isopentenyl transfera... | 36.8 | 0.005 |
| gnl\|CDD\|10515 | COG0645, COG0645, Predicted kinase [General function predictio... | 36.5 | 0.007 |

---

gnl|CDD|10198, COG0324, MiaA, tRNA delta(2)-isopentenylpyrophosphate transferase [Translation, ribosomal structure and biogenesis]

CD-Length = 308 residues, 85.4% aligned
Score = 226 bits (577), Expect = 5e-60

```
Query:  18   PLVVILGATGTGKSTLALQLGQRLGGEIVSADSMQVYEGLDIITNKVSAQEQRICRHHMI  77
Sbjct:  4    KLIVIAGPTASGKTALAIALAKRLGGEIISLDSMQVYRGLDIGTAKPSLEELAGVPHHLI  63

Query:  78   SFVDPLVTNYTVVDFRNRATALIEDIFARDKIPIVVGGTNYYIESLLWKVLVNTKPQEMG  137
Sbjct:  64   DIRDP-TESYSAAEFQRDALAAIDDILARGKLPILVGGTGLYLKA-LLEGLSLLPEADPE  121

Query:  138  TEKVIDRKVELEKEDGLVLHKRLSQVDPEMAAKLHPHDKRKVARSLQVFEETGISHSEFL  197
Sbjct:  122  VRRRLEA--ELAELGNDALHAELKKIDPEAAAKIHPNDPQRIIRALEVYYLTGKPISELQ  179

Query:  198  HRQHTEEGGGPLGGPLKFSNPCILWLHADQAVLDERLDKRVDDMLAAGLLEELRDFHRRY  257
Sbjct:  180  KRSRPILEPY---------DILIIALAADREVLYERINRRVDAMLEQGLIEEVKALYARG  230

Query:  258  NQKNVSENSQDYQHGIFQSIGFKEFHEYLITEGKCTLETSNQLLKKG  304
Sbjct:  231  LHLD---------LPAMQAIGYKEILAYL--DGGISLEEAIERIKTA  266
```